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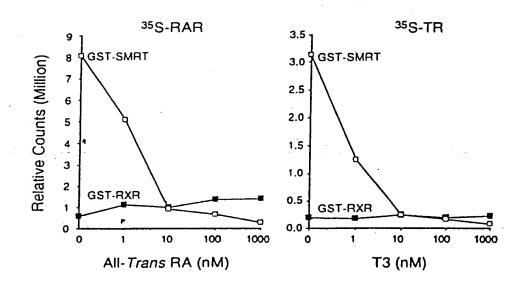


FIGURE 1

A FAMILY OF TRANSCRIPTIONAL CO-REPRESSORS THAT INTERACT WITH NUCLEAR HORMONE RECEPTORS AND USES THEREFOR – Evans et al. – 09/522,753 – Sheet 2 of 13

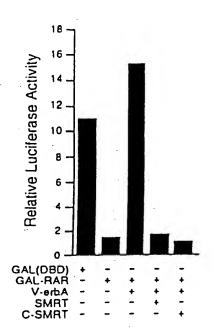


MEAWDAHPDKEAFAAEAQKLPGDBBCWTSGLPFBVPPREVIKASPHAPDB SAFSYABBGHBLBLGLHDTARPVLPRPPTISNPPPLISSAKHPSVLERQI GAISQGMSVQLHVPYSEHAKAPVQPVTMGLPLPMDPKKLAPFSGVKQEQL SPRGOAGPPESLGVPTAOEASVLRGTALGSVPGGSITKGIPSTRVPSDSA 151 ITYRGS ITHGTPADVLYKGT ITR I IGEDS PSRLDRGREDSLPKGHV I YEG 201 KKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAI 251 SSASIEGLMGRAIPPERHSPHHLKEQHHIRGSITQGIPRSYVEAQEDYLR 301 REAKLLKREGTPPPPPPSRDLTEAYKTOALGPLKLKPAHEGLVATVKEAG RSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHD **VRSLIGSPGRTFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSI** 451 **ARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEG** SLSSSKASODRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVSGVD LYRSHIPLAFDPTSIPRGIPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRG YPDTAALENRQTIINDYITSQQMHHNTATAMAQRADMLRGLSPRESSLAL 701 NYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPOPFSSRH SSSPLSPGGPTHLTKPTTTSSSERERDRDRERDRDREREKSILTSTTTVE HAPIWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPISPRTQDALQ ORPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLG GTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPA 901 SSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASASDPH REKTQSKPFSIQELELRSLGYHGSSYSPEGVEPVSPVSSPSLTHDKGLPK 1001 HLEELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQT 1051 APGVKGHQRVVTLAQHISEVITQDYTRHHHQQLSAPLPAPLYSFPGASCP VLDLRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGI 1151 EPVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFF SKITESNSAM/KSKKQEINKKLNTHNRNEPEYNISQPGTEIFNMPAITGT 1301 GLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQW.EESPPLSANAFNPL NASASLPAAMPITAADGRSDHTLTSP. GGGGKAKVSGRPSSRKAKSPAPG 1350 LA..SGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPL MRLQAGMASPPPPGLPAGSGFL. . AGPHHA. . . WDEEPKPLLCSQYETL



FIGURE 3A

FIGURE 3B



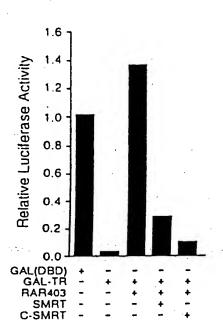
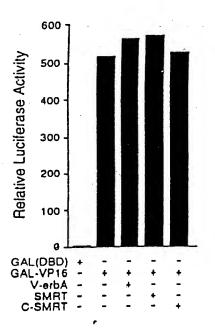
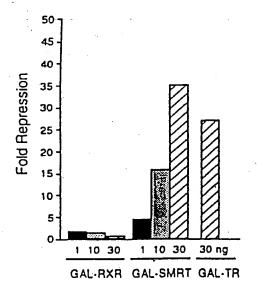


FIGURE 3C

FIGURE 3D





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A FAMILY OF TRANSCRIPTIONAL CO-REPRESSORS THAT INTERACT WITH NUCLEAR HORMONE RECEPTORS AND USES THEREFOR. – Evans et al. – 09/522,753 – Sheet 4 of 13

MSGSTQLVAQTWRATEPRYPPHSLSYPVQIARTHTDVGLLEYQHHSRDYASHLSPGSIIQPQRRRPSLLSEFQPGNERSQELHLRPESHSYLPELGKSEM MSGSTQPVAQTWRAAEPRYPPHGISYPVQIARSHTDVGLLEYQHHPRDYTSHLSPGSIIQPQRRRPSLLSEFQPGSERSQELHLRPESRTFLPELGKPDI

		•
101 101	${\tt EFIESKRPRLELLPDPLLRPSPLLATGQPAGSEDLTKDRSLTGKLEPVSPPSPPHTDPELELVPPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLELLPDTLLRPSPLLATGQPSGSEDLTKDRSLAGKLEPVSPPSPPHADPELELAPSRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLELLPDTLLRPSPLLATGQPSGSEDLTKDRSLAGKLEPVSPPSPPHADPELELAPSRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLELLPDTLLRPSPLLATGQPSGSEDLTKDRSLAGKLEPVSPPSPPHADPELELAPSRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLELLPDTLLRPSPLLATGQPSGSEDLTKDRSLAGKLEPVSPPSPPHADPELELAPSRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLELLPDTLLRPSPLLATGQPSGSEDLTKDRSLAGKLEPVSPPSPPHADPELELAPSRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLELLPDTLLRPSPLATGQPSGSEDLTKDRSLAGKLEPVSPPSPPHADPELELAPSRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLELLPDTLLRPSPLATGQPSGSEDLTKDRSLAGKLEPVSPPSPPHADPELELAPSRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLELLPDTLLRPSPLATGQPSGSEDLTKDRSLAGKLEPVSPPSPPHADPELELAPSRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLELLPDTLLRPSPLATGQPSGSEDLTKDRSLAGKLEPVSPPSPPHADPELELAPSRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLSKEELIQNMDRVDREITMVEQQISKLKKKKQQQL}\\ {\tt EFTESKRPRLSKEELIQNMDRVDREITMVEQQISKLKKKKQQQL}\\ {\tt EFTESKRPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL}\\ {\tt EFTESKRPRLSKEELIQNMDRVDREITMVEQQISKLKKQQQL}\\ {\tt EFTESKRPRLSKEELIQNMDRVDREITMVEQQISKLKKQQQL}\\ {\tt EFTESKRPRLSKAGAR}\\ {$	
201 201	${\tt EEEAAKPPEPEKPVSPPPIESKHRSLVQIIYDENRKKAEAAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKPCQ\\ {\tt EEEAAKPPEPEKPVSPPPIESKHRSLVQIIYDENRKKAEAAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWEQRFCQ\\ {\tt CONTROL OF CONTR$	
301 301	$\label{eq:rydolmealekkveriennprrakeskvreyyekoppeirkoreloermosrvoorgsglsmsaarsehevseiidglseoenlekomrolavippmly\\ \text{Rydolmeawekkveriennprrakeskvreyyekoppeirkoreloermosrvoorgsglsmsaarsehevseiidglseoenlekomrolavippmly}$	
401 401	${\tt DADQQRIKFINMNGLMADPMKVYKDRQVMNMWSEQEKETPREKFMQHPKNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVRRSYRRGKSQQQQQQQQQDQDDADQQRIKFINMNGLMDDPMKVYKDRQVTNMWSEQERDTPREKFMQHPKNFGLIASFLERKTVAECVLYYYLTKKNENYKSLVRRSYRRGKSQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ$	
501 501	$QQQQQQQQQPMPRSSQEEKDEKEKEAEKEEEKPEVENDKEDLLKEKTDDTSGEDNDEKEAVASKGRKTANSQGRRKGRITRSMANEANSEEAITPQQ\\QQQQQQQmarssqeekeekekekeadkeeekQdaenekeelskektddTsGednhekeavaskGrktansqGrrkgritrsmaneanheetatpQQ\\$	
601 597	SAELASMELNESSRWTEEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQQHKLKMEKERNARRKKKKAPAAASEEAAFPPVV SSELASMEMNESSRWTEEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQQHKLKMEKERNARRKKKKTPAAASEETAFPPAA	
701 697	${\tt EDEEMEASGVSGNEEEMVEEAEALHASGNEVPR-GECSGPATVNNSSDTESIPSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPPRRTSRAPIEPTPA\\ {\tt EDEEMEASGASANEEELAEEAEASQASGNEVPRVGECSGPAAVNNSSDTESVPSPRSEAMKDTGPKPTGTEALPAATQPPVPPPEEPAVAPAEPSPV}$	
800 794	SEATGAPTPPPAPPSPSAPPPVVPKEEKEEETAAAPPVEEGEEQKPPAAEE-LAVDTGKAEEPVKSECTEEAEEGPA-KGKDAEAAEATAEGALK PDASGPPSPEPSHHLPH-PRLLWTRMNKKPRLLQLPRQRMPRSRSLRPRRSMWEKPEEPEASEEPPESVKSDHKEETEEEPEDKAKGTEAIETVSEAPLK	
893 893	AEKKEGGSGRATTAKSSGAPQDSDSSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANASPQKPLDLKQLKQRAAAIPPIQVTKVHEPPREDAAPT VEE-AGSKAAVTKGSSSGATQDSDFSATCSADEVDEPEGGDKGRLLSPRPSLLTPAGDPRASTSPQKPLDLKQLKQRAAAIPPIQVTKVHEPPREDTVPP	
993 992	KPAPPAPPPPONLQPESDAPQQPGSSPRGKSRSPAPPADKEAFAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPL KPVPPVPPTQHLQPEGDVSQQSGGSPRGKSRSPVPPAEKEAEKPAFFPAFPTEGPKLPTEPRWSSGLPFPIPPREVIKTSPHAADPSAFSYTPPGHPL	
	PLGLHDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQ-GMSVQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLAPPSGVKQEQLSPRGQAGPPES PLGLHDSARPVLPRPPISNPPPLISSAKHPGVLERQLGAISQQGMSVQLRVPHSEHAKAPMGPLTMGLPLAVDPKKL	
	LGVPTAQEASVLRGTALGSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGGTALGSATSGSITKGLPSTRAADGPSYRGSITHGTPADVLYKGTISRIVGEDSPSRLDRAREDTLPKGHVIYEGKKGHVLSYEGG	
	${\tt MSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGT\\ {\tt MSVSQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRTVTSASIEGLMGRAIP-EQHSPH-LKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGT\\ {\tt MSVSQCSKEDGRSSGPPHETAAPKRTYDMMEGRVGRTVTSASIEGLMGRAIP-EQHSPH-LKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGT\\ {\tt MSVSQCSKEDGRSSGPPHETAAPKRTYDMMEGRVGRTVTSASIEGLMGRAIP-EQHSPH-LKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGT\\ {\tt MSVSQCSKEDGRSSGPPHETAAPKRTYDMSGRTVTSASIEGLMGRAIP-EQHSPH-LKEQHHIRGSITQGIPRSYVEAQEDYLREAKLLKREGT\\ {\tt MSVSQCSMSGRTYDMSGRT$	h-SMRT m-SMRT
	PPPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSLIGSP PPPPPPPRDLTETYKPRPLDPLGPLKLKPTHEGVVATVKEAGRSIHEIPREELRRTPELPLAPRPLKEGSITQGTPLKYDSGAPSTGTKKHDVRSIIGSP	h-SMRT m-SMRT
	GRTFPPVHPLDVMADARALERACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSSKAS GRPFPALHPLDIMADARALERACYEESLKSRSGTSSGAGGSITRGAPVVVPELGKPRQSPLTYEDHGAPFTSHLPRGSPVTTREPTPRLQEGSLLSSKAS	h-SMRT m-SMRT
	${\tt QDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVSGVDLYRSHIPLAPDPTSIPRGIPLDAAAA-YYLPRHLAPNPTYPHLYPPYLIRGYPDTAAL\\ {\tt QDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVTGVDLYRGHIPLAPDPTSIPRGIPLEAAAAAYYLPRHLAPSPTYPHLYPPYLIRGYPDTAAL\\ {\tt QDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVTGVDLYRGHIPLAPDPTSIPRGIPLEAAAAAYYLPRHLAPSPTYPHLYPPYLIRGYPDTAAL\\ {\tt QDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVTGVDLYRGHIPLAPDPTSIPRGIPLEAAAAAYYLPRHLAPSPTYPHLYPPYLIRGYPDTAAL\\ {\tt QDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVTGVDLYRGHIPLAPDPTSIPRGIPLEAAAAAYYLPRHLAPSPTYPHLYPPYLIRGYPDTAAL\\ {\tt QDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVTGVDLYRGHIPLAPDPTSIPRGIPLEAAAAAYYLPRHLAPSPTYPHLYPPYLIRGYPDTAAL\\ {\tt QDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRGVTGVDLYRGHIPLAPDPTSIPRGIPLEAAAAAYYLPRHLAPSPTYPHLYPPYLIRGYPDTAAL\\ {\tt QDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLRGVTGVDLYRGHIPLAPDPTSIPRGIPLEAAAAAAYYLPRHLAPSPTYPHLYPPYLIRGYPDTAAL\\ {\tt QDRKLTSTPREIAKSPHSTVPEHPHPHPHPHPHPHPHPHPHPHPHPHPHPHPHPHPHPH$	h-SMRT m-SMRT
	${\tt ENRQTIINDYITSQQMHHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSPLSP\\ {\tt ENRQTIINDYITSQQMHHNAASAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGTPATAIDRLAYLPTAPPPFSSRHSSSPLSP\\ {\tt ENRQTIINDYITSQUPPTPGTPATAIDRLAYLPTAPPPFSSRHSPRESSPLSPPTPATAIDRLAYLPTAPPPPTSGRAMAQRADMLAYLPTAPPPTPGTPATATATATATATATATATATATATATATA$	h-SMRT m-SMRT
	GGPTHLTKPTTTSSSERERDRDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSGGGGSSSRPASHSHAHQHSPISPRTQDALQQRPSVLH GGPTHLAKPTATSSSERERERERERDKSILTSTTTVEHAPIWRPGTEQSSGAGGSSRPASHTHQHSPISPRTQDALQQRPSVLH	h-SMRT m-SMRT
	${\tt NTGMKGIITAVEPSKPTVLRSTSTSSPVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLEPASSPS\\ {\tt NTSMKGVVTSVEPGTPTVLRWARSTSTSSPVRPAATFPPATHCPLGGTLEGVYPTLMEPVLLPKETSRVARPERARVDAGHAFLTKPPGREPASSPS\\ {\tt NTSMKGVTSVEPGTPTVLRWARSTSTSPVRPATHCPLGGTLEGVYPTLMEPVLLPKTSTSPVRPATHCPLGGTLEGVYPTTVLRWARSTSPVRPATHCPLGGTLEGVYPTTVLRWARSTSPVRPATHCPLGGTLGGTLGGTLGGTVTTVLRWARSTSPVRPATHCPLGGTLGGTLGGTVTTTVLRWARSTSPVRPATHCPLGGTLGGTLGGTVTTTVLRWARSTSPVRPATHCPLGGTLGGTVTTTVLRWARSTSPVRPATHCPLGGTLGGTVTTTVLRWARSTSPVRPATHCPLGGTLGGTVTTTVLRWARSTSPVRTPATHCPLGGTLGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	
	${\tt KGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASASDPHREKTQSKPFSIQELELRSLGYH-GSSYSPEGVEPVSPVSSPSLTHDKGLPKHLE\\ {\tt KSSEPRSLAPPSSSHTAIARTPAKNLAPHHASPDPPAPT-SASDLHREKTQSKPFSIQELELRSLGYHSGAGYSPDGVEPISPVSSPSLTHDKGLSKPLE$	
	$\verb ELDKSHLEGELRPKQPGPVKLGGEAAHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRHHPQQLSAPLPAPLYSFPGASCPVLD \\ \verb ELEKSHLEGELRHKQPGPMKLSAEAAHLPHLRPLPESQPSSSPLLQTAPGIKGHQRVVTLAQHISEVITQDYTRHHPQQLSGPLPAPLYSFPGASCPVLD \\ \verb ELEKSHLEGELRHKQPGPMKLSAEAAHLPHLRPLPESQPSSPLQTAPGIKGHQRVVTLAQHISEVITQDYTRHHPQQLSGPLPAPLYSFPGASCPVLD \\ \verb ELEKSHLEGELRHKQPGMSSPLPAPLYSFPGASCPVLD ELEKSHQPTAPQTAPGIKGPTAPTAPTAPTAPTAPTAPTAPTAPTAPTAPTAPTAPTAP$	h-SMRT m-SMRT
	$LRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKL\\ LRRPPSDLYLPPPDHGTPARGSPHSEGGKRSPEPSKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQGEPR-MGLESPGNTSQPPTFFSKL\\ LRRPPSDLYLPPDHGTPARGSPHSEGGKRSPEPSKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQGEPR-MGLESPGNTSQPPTFFSKL\\ LRRPPSDLYLPPDHGTPARGSPHSEGGKRSPEPSKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQGEPR-MGLESPGNTSQPPTFFSKL\\ LRRPPSDLYLPPDHGTPARGSPHSEGGKRSPEPSKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQGEPR-MGLESPGNTSQPPTFFSKL\\ LRRPPSDLYLPPDHGTPARGSPHSEGGKRSPEPSKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQGEPR-MGLESPGNTSQPPTFFSKL\\ LRRPPSDLYLPPDHGTPARGSPHSGGKSPEPSKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQGEPR-MGLESPGNTSQPPTFFSKL\\ LRRPPSDLYLPPDHGTPARGSPHSGGKRSPEPSKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQGEPR-MGLESPGNTSQPPTFFSKL\\ LRRPPSDLYLPPDHGTPARGSPHSGGKRSPEPSKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQGEPR-MGLESPGNTSQPPTFFSKL\\ LRRPPSDLYLPPDHGTPARGSPHSGGKRSPEPSKTSVLGSSEDAIEPVSPPEGMTEPGHARSTAYPLLYRDGEQGEPR-MGLESPGNTSQPPTFFSKL$	h-SMRT m-SMRT
	TESNSAMVKSKKQEINKKLNTHNRNEPEYNISQPGTEIPNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPPLSANAFNPLNASA TESNSAMVKSKKQEINKKLNTHNRNEPEYNIGQPGTEIPNMPAITGAGLMTCRSQAVQEHASTNMGLEAIIRKALMGKYDQWEEPPPLGANAFNPLNASA	h-SMRT m-SMRT
	${\tt SLPAA-MPITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGSLPAAAMPITTADGRSDHALTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGSTPAAAMPITTADGRSDHALTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGSTPAAAMPITTADGRSDHALTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGSTPAAAMPITTADGRSDHALTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGSTPAAAMPITTADGRSDHALTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGSTPAAAMPITTADGRSDHALTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGSTPAAAMPITTADGRSDHALTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTPFPYNPLIMRLQAGSTPAAAMPITTADGRSDHAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG$	h-SMRT m-SMRT
	VMASPPPPGLPAGSGPLAGPHHAWDEEPKPLLCSQYETLSDSE VMASPPPPGLAAGSGPLAGPHHAWDEEPKPLLCSQYETLSDSE	h-SMRT m-SMRT
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A FAMILY OF TRANSCRIPTIONAL CO-REPRESSORS THAT INTERACT WITH NUCLEAR HORMONE RECEPTORS AND USES THEREFOR – Evans et al. – 09/522,753 – Sheet 5 of 13



hM-COR hN-CoR HN-COR hN-CoR hN-CoR h-SMRT h-SMPT h-SMRT hu-Cob h-SMRT h-SMRT h-SMR7 hN-CoR hN-CoR h-SMRT hN-CoR hN-COF ГКИ ЮФЙЯККІЛЬГКЯКИНАКСФОВТООГНЕФБЕККУРЕТЕМИРЕВФКЕКУЕКОЕТЕКОРЕТЕКОВЕТЕКОВЕДЕВГОВВООВЯЗІТЯНЗАВЛЕВБЕТТООГЯБОБИ БООВИ 110 МУФЙЯККІЛЬГЕККВИНАКСФРООКУРООГНЕФБККУФРІДЕМИРЕВФКЕКУВКОГРЕТЯКОВЕФВЕЮ РОСОВОРОЗЭТ ТАКІВНЯ ВЕТІЛОДЬБОВУБСОВУБСОВУБСОВУБОВНІВ В РРУVРКЕВКЕЕЕТАЛАРРИЕВОВВОКФРИВЕЦИЙГОКИВЕТЕВЕВЕВОРАКТИВБИВАТИВБИВАТИВОВИЛА ТИКSSOAROTOSTESTESTESTESTESTESTORY -------EDHUVDOOBHSA<u>EES</u>SVCI<u>EPF</u>BIK--ADSVDVEHUBEKVESDVTKSBUNTKSRUD. DABSBKVEP ------EDHUVDOOBHSA<u>EESSVCEP-EKCEP</u>FFFUSKE<u>PFDLAGSILVSS</u>FLVSSP -рокФЕЛІКОВХАДГРВІООТКИНЕРРВЕВЛАНТКРАРРАРРРРОКЦ-ОРЕБЕДФООРДЗБРЯВКЯКВРАРРАЛЬТАЛЕЛОКІНГОНДЗ-1. РИЗВИДРВУДІЗ----ОТПИЦРЯДУВДУДІВ-----ЦИКВ LKPHR<u>LODIKDIOHDANIETI</u>V-------SCTBT-NIPIGTEVSGYALMQRH1M5NH1M5NH1M5NH1M5NH1M5NH1M2H1M2H1M2H1M2H1M2H1M2H1M2H1M2H1M3 VMADA-RALEBAÇIB ----EBLEFRPOTASSGISTARIADVIVEBLGFPROSTATIVDIGA ----PFAGHLFFGSTATNFPEPTRLOEGSLSSSKASOGFR ----EBLFFRBLAKSPIGTVFBHFFN-PJSTYEDVIRG IVPENIKVOEBNIKVOEBNIKEVERNIKERISTLIFIJEDA SIPANSFYJOVIÐVVSHSIFOPHIKG Юйрвууйлосоправий циврэтреребейр габа из клом порти прикажен прикажен прикажен порти прикажен поставующей поста Койрвуттерней цистем протика при прикажен прикажен прикажен прикажен прикажен прикажен протисти прикажен при прикажен при GSPD-IRTRELATIVE PVSHPSPPT-OPELELAFPRLSKEELTQ-MUKVUREJTA-VECOJI-SKLKKKOOOLEEEAARPEPERFVSPPPPPRIKKASUVOI IYDENRKKABAAHII, EGIGAQVELPLYNOPSDTAQTHEN ASPONAYDA-GIKJENGSTOROODONAGISKV. EKEELLGSUDRUDREJAAVEOOJI (ALKKKOOOLEEBAARPEPERPVSPPPAKIKISI VOI IYDENRKKABAAM PEGIGBAVELPLYNOFSDIAVAHEN <mark>ОТРА, -------</mark>DAJEGATITARI JGEDSPSRLDRIKEDSLFRGHVIVEGRAGHALSYBGGMSVTOCSREDGRIGSGOPFHBTAARKRIFDRMEGRVORAJGI ------БАБЈЕGTJAGFAHPPFRP FRPI-HCKBJHH HGSTJF <u>OTPA</u>-POTOIPTEALMAGGLJEBPPIEDSSP--EKIRESAASKGH<u>VIVEG</u>KSJHILEXDNIKA----ARESTRSPRTA-HBISI-KOSKSJARGGARESFVSABPIEGJIAGALEJ-BISPLAKBYTVASGSJA 2148 TRIHPOOLSAPJAARIVSEPOASCOVID-- IMAPPEDITJEPPD-----HGAPARISEBOOTA ENPERINGENIGHESTEREPERINGSTEPPENISPEPALISE 2064 ARHOVSS-OURDOFFIFTISPSALVSTPURIKTENTYJEPSOAOSVIHORPOSBJEJENLVIKERISEPSERSKYSSEPYERIERIEPIG--VPVVIBKOOSLILLISORJAEPAROGSOAOSVIHORPOSBJEJEPELJE 2270 XISHWKKKOBI KKCAHINKKEBEYNIGOPGTEIFM/PAUTHIGJMTYRSOAVOEHAGIMGIEMLIRKALKKYDDWEBSPLSAHARNPINASASLPAAMPITHADGRDHTLISTGGGG--FPRVSGRESFRYRR 2200 VIGHWKSKKQBI FRILLISSGGGDSDWAAYO<u>PGTEIFM</u> PAYLISGSVSGRSHSFADFAG-BJ<u>ALB</u>DLIRKALMGSFDDKVBDHGVYMS---QPAGVVPGTANTSVYLBGGTRREGDFSBHSGGVQFKJ.ISKSH<u>SRIFK</u> ERNEGA---saufilisivssuuseadyngalipunnnumeerssaastappinnelumelaaavnaspeerakaasaen--lajeha---moeernellessessaa Silvegaviotieressassaassaansaabyngaliji-ammeerssaastappinnelynnelumee---lasheerraassavaaapannilysmeerpeulenoie 1095 1168 1357 1492 1422 1618 1298 1232 1793 2416 1896 549 126 410 619 194

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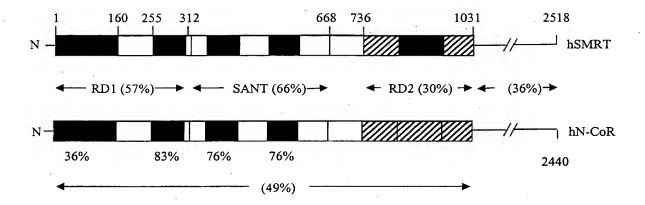


FIGURE 5B



FIGURE 6A

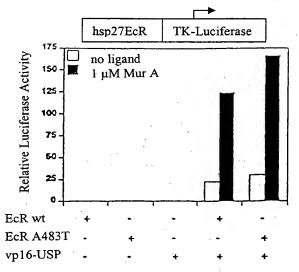


FIGURE 6B

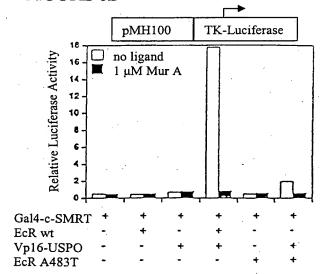
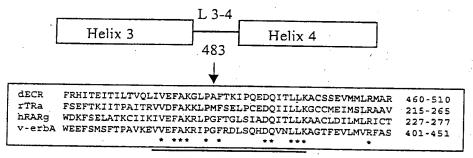


FIGURE 6C



LBD-signature Motif



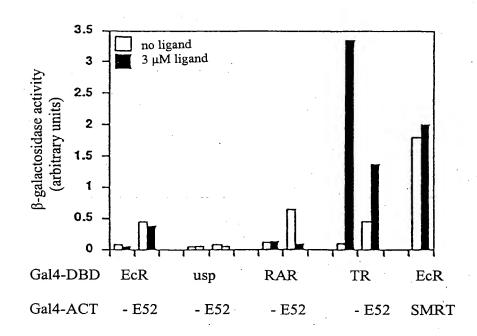


FIGURE 7



1 MSAYQQRLPSNAASIHSPHWSYRALEQQQQYAKQAAHLQQQQQQQQQQQQQQQQQQQQQQTNLHLQIHHHHQQQQQQQQQQQQQ 81 QQQQQQQQQQQQQQQEHMQQQQQQQLSPPHPPGSS5NSSSAAAAAAAAAAAAAAAVNPGYPPSSAAAAAAAAAAVNSGYPPRPPQ 160 161 ERFIQHTGYSIAPAPTYRDHPYSRHTQIQQQQQQQQQQQQQQQQQQQQQAAASHPEYQRAAARAAVAAVSAGKGHVS 240 241 GQSSNSSSSSSGGGGGGGSAGGSAPPGGGVVQV8QSGGVLVMEAMPHYASQPNSNPSQQQQQQQQQQQGGNPSGAGATSG 320 321 AGGGGGGSGSVMVGSLGRILMPHPQALQYTSEYLTNATAAVAAANVNQRQHLQLQQQQQQQHPPEPFGGQQPYKKQRLS 400 401 EANANNMHLPPHPQQQHQQQQQQQBQRSSPAQVQQQQQQMNSSRQSHNDMCRQVVTTPMGMQLKVETLPQQQQKQQ 480 481 QHQQQQQQQQGRSQPVVSSMSTVVSQPVGTVTVTTAGLSASHSGSSGNVAAGLGTGNTGSASTRAYHPQVZAISPTLPS 560 561 DSSIEERGRTS<u>AKEDLIMOIOKYDNEIKSAETTHETLRKKEKSIMEEAALAKEORAAKELNDMNNDOEPHVELSWRSOMI</u> 640 641 AEKIYAANRKTAOAOHSMLONAAADESSPGSYAGRPWLPLYNOPLDVEALAMLIROHOSOIRAPLLLHIRKLKAERWAEN 720 721 <u>OGLVEKYTKDOADWORRCERMEASAKRKAREAKNREFFEKYPTELRKOREDKERFNRYGSRIKSEADLEEIMDGLOEOAL</u> 800 801 EDKKMRSYAVIPPLAHDARORRCAYHMENGLIEDMYAYHOORKALAMWTAGEKETFKEKYLOHPKNFGALAASLDRKSPO 880 881 <u>DCYRYXLSKATENYK</u>OLLRKSRORTRSSRNPAKAQAAQPQCIIDSMTTGVMTRLQREQQQKSGGRSSAVAERERAERAA 960 961 Erekvaekaaadaakaaesaaekasaatkaveataagekvakaaaaaaaaaaattattattattatsssesssssssastas 1040 1041 estaspatlagiaadrtdagrtasasdrnaataogptatgtptaattpatatapppeieaogparsknappelaaatagaat 1120 1121 VATAGTPATGASAASAGEATTATGATATAAAKGVCKPETATEPAGTAAKGADSRPDANDPLAKTASKAINAEGYNAIGON 1200 1201 essseskatgasapvqgvtlmgfkpgtqtvvmrbykaetogddsganaqqaapgslaatmaslategdkivkttpesrap 1280 1281 estsstännesssgagvetygetättageylogklkaagveglgagnelesdvseskrkrfelnsgeagghatsamtess 1360 1361 tsgsknienseglkanakdgsknaktenastesaevvytetpsaeesslesaasklieaaevkstaagatesetattta 1440 1441 tasaislpiladgsghshvhaheilaldgkdklascfyckaeacprtrplkkgrgqqygipdetipagarychscqcksy 1520 1521 RSRYPRCPLPTCPNPKDRAQRLRNIPSRLFELAPEVRDPLMAEFQIPPHATRCCSACLMRIRRKLDPQLNLTDGSSGGAG 1600 1601 BGSGGDETDVSTSSCDEREPOGSDTABVESPENLQRHKSLTMVKQQQQQQQQQQQQQQQQQQQQQLGQPQPPPPAPQQ 1680 1681 QKGSSGRGCDQGTPLIITPTRMSSKSGSGQAQTAGDMERLLPPAAGQAPKKQKTSKEYDSSATETADEENENSPAMRQSP 1760 1841 Q0QQQQQQQQQQQQQQTPQQSQSFSQQQQQQQQQQSABBLERKKLTIVREYRQDPGILKQQQQQQQQAGGAPPTSAAGSL 1920 1921 PEGTSVQKLTTRPAAVAPPPPAEPLTPTSIGCAGENEGTEDSLATLSVVESEEMGKVGIGEPGPHAEASSAGGIGVDKATI 2000 2001 TPVVKSSGSSKSGGGSASSHSTATPPETIITEVPVAHPQRGIPPPSQHSVHPAHPSHTQHPAHPQHSSHQQHTQLQVPE 2080 2081 PEPOTLDLSIKKPPRDCHSPHTGAGGSSSSGSBGGP88SDRHGGPPPPTMSHKHIVRSGCMYRGDTVTVPSLAAPSSYL 2160 2161 YPTRSVKSIGGGGVVPGVLPGVPGIALYLQPVPVPVPISIGGQGQLPPKAGQPPPAQPPSGRGVAKVPPKLSPQQAHHLH 2240 2241 PSHGESPSQQQQQQQQQQQQQQQAAAAAQQQLLVKSG<u>SIIEGTP</u>ANSAQQQIIVHAPATAAAAPSSLFSFKFDGLVRQTT 2320 2321 PECVOSVOPOGASCSCKEGSITOGTPLENPPEHLESKRPYESYYKSSQRESPAQQPGCNQQLPPPPQQSSPQAPPPQGYG 2400 2401 YGV85PYAR3PFAGYVEQPQVL3<u>TRQIYMEDYITSOOM</u>OQQQQQQQQQQQQQRMHSRGSSAGGGGGGGSDKE3PSPRNS 2480 2481 VGSASGYAYGGDKESAPRGRPKYSSRASPADHVNSTPSPERTPPPQRQGVIQRENTGSKPPSPAAPPPSRMENDPYQYAP 2560 2561 SGEDALASYVDVAVQQPQLPVPSQKDDKSPGPSTAPGQVPGSGPPLGPSPLPPEAVVOVAQPPPPTAEEDQRTRDLTLEH 2640 2641 BEHTLYQQQIAQQQHYRSLNYAAQYDMQRQMDQAKRYMRHQQHQYQQQQQQQQQQQQHNHALERDREHQERH<u>RERDRERER</u> 2720 2721 EREREGREREREREREREREREDBARRYVALEREBDSRRMERMFAGNYVTGSGGAGGGGPSPGQFLRASVPETGPP 2600 2801 RSIPDRERESYYRQAHGGPAPEDTPCQLSAQSLIDAIIXHLINRSNDATAGPGREFPRPSFVHAPLPPRGSGSGGGTGTR 2880 3281 RESACSOSVSYSYGGANSHBERYHPPANNYAS TAYYANYYGANGGIPPEGYYQIAEGAYAPPGAYAKAKAAHALS 3360 3361 Elgavoggyslvvgggsgglaggpggysvgygypggogpgsoogggginssssgasaavaaas<u>eskplilskyd</u> 3440 3441 <u>ALSDED</u>*

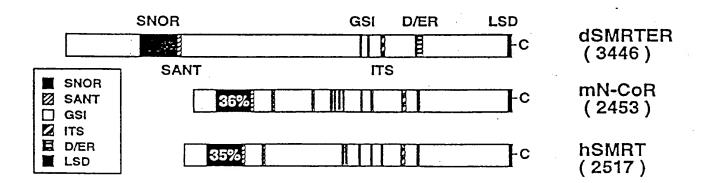


FIGURE 8B

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TRADEMARY SNOR motif 1.0 20 3.0 4 0 5 0 SMRTER: KEDILIMOIOKV DNE IKSAETTMETURKKEKSIMEEAALAKEORAAKELND 573 KEELIOSMDRVDREIAKVEQOILKLKKKQQOLEEEA - AKPPEPEKPVSP KEELIONMDRVDREITMVEQOISKLKKKQQOLEEEA - AKPPEPEKPVSP mN-CoR: 377 hSMRT : 169 60 70 8 0 90 3.0.0 NUNDOEPMVELSWRSOMLAEKT YAANRKTADA CHSMLONAA ADESSPGSV SMRTER: 623 ---PPVEOKHRS--IVOIIYDENRKKAEEAHKIFEGLGPKVE mN-CoR: 226 hsmrt : 217 PPIESKHRS--LVQIIYDENRKKAEAAHRI LEGLGPOVE 120 110 140 150 SMRTER: 673 AGREWLPLYNOFLDVEALAMUIROHOSOIRAFLILHIRKLKAERWAHNOG -LPLYNOPSDTKVYHENIKINON - MRKKLILIFKRRNHARKOREOK -LPLYNOPSDTROYHENIKINOA - MRKKLILIFKRRNHARKOWKOK mN-CoR: 263 hSMRT : 254 160 170 180 190 LVEKYTKDOADWORRICERMEASAKRKAREAKNREFFEKVFTELRKOREDK ICORYDOLMEAWEKKVDRIENNPRRKAKESKTREYYEKOFPEIRKOREDO SMRTER: 723 mN - CoR : 307 FCORYDOLMEADEKKVERIENNPRRAKESKVREYYEKOFPEIRKORELO hsmrt . 298 210 220 230 240 SMRTER . 773 ERFN-RVGSR------IKSEADLEEIMDGLOEOALEDKKMRSYAVIPP ERFO-RVGQRGAGLSATIARSEHEISEIIDGLSEQENNEKOMRQLSVIPP ERMOSRVGQRGSGLSMSAARSEHEVSEIIDGLSEQENLEKOMRQLAVIPP mN-CoR: 357 hSMRT : 348 270 260 280 LMHDARORRCAYHNENGLIEDMVANHQORKALNM MMFDAEDRRVKFINMNGLMEDPMKVYKDROFMNV SMRTER: 814 mN-CoR: 406 hsmrt : MUYDADDDRIKFINMNGLMADPMKVYKDROMMNM 398 **SANT domain** 10 20 30 WTAGERETFKERYLOHPKNFGALAASUDR-KSPODCVRYYYLSKKTENY 100%
WTDHEKELFROKFIOHPKNFGLLASYLER-KSVPDCVLYYYLTKKNENY 68/80%
WSEQEKETFREKFMOHPKNFGLLASFLER-KTVAECVLYYYLTKKNENY 64/82%
WSPEERSLFKSROADHVKLFHGLTEFFVD-KTASDLVLFYYMNKKTEDW 35/53%
WTPDELYOFODALYOSEKDFDKVANELPG-KSVKECVOFYYTWKKDCPD 38/56%
WTEEECRNFEQGLKALGKDFHLLOANKVRTRSVGECVAFYYMWKKSERV 36/56%
WTEEEMEVAKKGLVEHGRNWAALAK-MVGTKSEKOCKNFYFNYKRRHNL 34/53%
WTEEEMETAKKGLLEHGRNWSALAR-MVGSKTVSQCKNFYFNYKKRONL 38/57%
WTVKDKVLFEQAFSFHGKFFHRLOOMLPD-KSLASLVKFYYSWKKTRTK 37/50%
WTDDELTLFENCYQLFGKNFSQLRSALCH-RSLOSLVOFYYESKKRVKV 39/51%
FTDHEHSLFLEGYLLHEKKFGKLSHVMGGLRSPEECVLHYYRTKKTVNY 46/62% SMRTER :848 mN-CoR(1):440 hSMRT(1) :432 c14B9.6 :615 cF53H10 :218 :277 mN-CoR(2):627 hSMRT(2) :615. hKIAA0071:106 CMTA-I :198 YCR592 :673 α-helix α−helix ITS motif GSI motif SMRTER: 2424 TROIVMHDYITSQOMO SMRTER: 2274 VKSGSIIHGTPANS SMRT:1681 NROTTINDYITSOOMH GKHGSITOGTPLHM VPGGSITKGIPSTR TYRGSITHGTPADV 2236 N-CoR:1615 TROTILNDYITSOOMO SMRT: 1203 1224 1350 HIRGSITOGIPRSY 1446 LKEGSI<u>TO</u>GTPLKY SSGGSIARGAPVIV TPPGSILISSPIKP 1517 N-COR: 921 1064 IMGGSISOGTPGTY LSD motif PSVGSISTGLPRQQ 1092 VOEGSITRGTPASK 1149 1171 SLRGSITOGTPALP ESKPLLLSKYDALSD-ED SMRTER: 3430 1302 VLSGSIMOGTPRAT SMRT:2501 1388 IIEGSISOGTPIKF EPAPLLSADYETLSDSDD N-CoR:2436 C14B9.6: QTQGSLTSGTPFQA 920



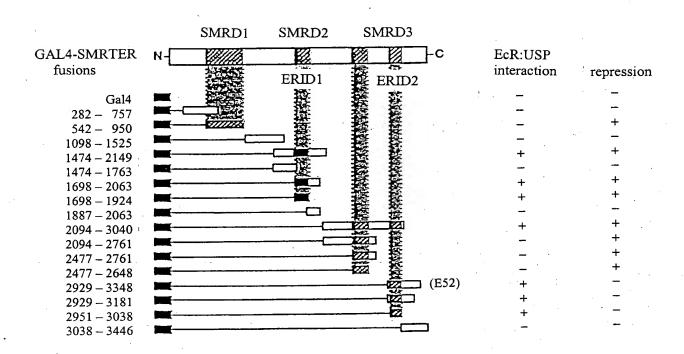


FIGURE 10



